



# SEQUENCE LISTING

<110> Schutte, Brian C.  
Murray, Jeffrey C.  
Kondo, Shinji  
Dixon, Michael J.

<120> IRF6 POLYMORPHISMS ASSOCIATED WITH CLEFT LIP AND/OR PALATE

<130> P06215US01

<140> US  
<141> 2004-05-06

<150> US 60/468,191  
<151> 2003-05-06

<160> 4

<170> PatentIn version 3.3

<210> 1  
<211> 2171  
<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> (215)..(215)

<220>  
<221> variation  
<222> (216)..(216)  
<223> Frame shift to encode a MET. A to T (exon 2).

<220>  
<221> variation  
<222> (216)..(216)  
<223> Shift to encode alternate MET. A to T (exon 2).

<220>  
<221> CDS  
<222> (264)..(1667)

<220>  
<221> variation  
<222> (266)..(266)  
<223> G to A (exon 3)

<220>  
<221> variation  
<222> (268)..(268)  
<223> C to T (exon 3)

<220>  
<221> variation

<222> (280)..(280)  
 <223> 17ins(C) (exon 3)

<220>  
 <221> variation  
 <222> (312)..(312)  
 <223> 49del (CAGGTGGATAGTGGCC (exon 3)

<220>  
 <221> variation  
 <222> (315)..(315)  
 <223> G to A (exon 3)

<220>  
 <221> variation  
 <222> (316)..(316)  
 <223> T to C (exon 3)

<220>  
 <221> variation  
 <222> (332)..(332)  
 <223> C to A (exon 3)

<220>  
 <221> variation  
 <222> (378)..(378)  
 <223> C to G (exon 3)

<220>  
 <221> variation  
 <222> (441)..(441)  
 <223> T to G (exon 4)

<220>  
 <221> variation  
 <222> (460)..(460)  
 <223> C to G (exon 4)

<220>  
 <221> variation  
 <222> (465)..(465)  
 <223> C to T (exon 4)

<220>  
 <221> variation  
 <222> (471)..(471)  
 <223> G to C (exon 4)

<220>  
 <221> variation  
 <222> (489)..(489)  
 <223> C to T (exon 4)

<220>  
 <221> variation  
 <222> (507)..(507)  
 <223> C to A (exon 4)

<220>  
 <221> variation  
 <222> (513)..(513)  
 <223> C to T (exon 4)

<220>  
 <221> variation  
 <222> (514)..(514)  
 <223> G to A (exon 4)

<220>  
 <221> variation  
 <222> (525)..(525)  
 <223> A to C (exon 4)

<220>  
 <221> variation  
 <222> (528)..(528)  
 <223> A to G (exon 4)

<220>  
 <221> variation  
 <222> (531)..(531)  
 <223> A to G (exon 4)

<220>  
 <221> variation  
 <222> (537)..(537)  
 <223> G to T (exon 4)

<220>  
 <221> variation  
 <222> (555)..(555)  
 <223> G to C (exon 4)

<220>  
 <221> variation  
 <222> (615)..(615)  
 <223> C to T (exon 4)

<220>  
 <221> variation  
 <222> (729)..(729)  
 <223> 466ins(C) (exon 5)

<220>  
 <221> variation  
 <222> (821)..(821)  
 <223> C to A (exon 6)

<220>  
 <221> variation  
 <222> (839)..(839)  
 <223> G to A (exon 6)

<220>

<221> variation  
 <222> (897)..(897)  
 <223> 634ins(CCAC) (exon 6)

<220>  
 <221> variation  
 <222> (920)..(920)  
 <223> 657del(CTCTCTCCC)ins(TA) (exon 6)

<220>  
 <221> variation  
 <222> (1007)..(1007)  
 <223> 744del(CTGCC) (exon 7)

<220>  
 <221> variation  
 <222> (1012)..(1012)  
 <223> G to A (exon 7)

<220>  
 <221> variation  
 <222> (1022)..(1022)  
 <223> T to A (exon 7)

<220>  
 <221> variation  
 <222> (1058)..(1058)  
 <223> 795del(C) (exon 7)

<220>  
 <221> variation  
 <222> (1081)..(1081)  
 <223> A to G (exon 7)

<220>  
 <221> variation  
 <222> (1105)..(1105)  
 <223> 842del(A) (exon 7)

<220>  
 <221> variation  
 <222> (1133)..(1133)  
 <223> 870del(CACTAGCAAGCTGCTGGAC)lns(A) (exon 7)

<220>  
 <221> variation  
 <222> (1144)..(1144)  
 <223> T to C (exon 7)

<220>  
 <221> variation  
 <222> (1152)..(1152)  
 <223> G to A (exon 7)

<220>  
 <221> variation  
 <222> (1221)..(1221)

<223> A to G (exon 7)

<220>

<221> variation

<222> (1224)..(1224)

<223> G to A (exon 7)

<220>

<221> variation

<222> (1237)..(1237)

<223> G to A (exon 7)

<220>

<221> variation

<222> (1297)..(1297)

<223> T to C (exon 7)

<220>

<221> variation

<222> (1303)..(1303)

<223> G to T (exon 7)

<220>

<221> variation

<222> (1369)..(1369)

<223> T to C (exon 8)

<220>

<221> variation

<222> (1385)..(1385)

<223> C to G (exon 8)

<220>

<221> variation

<222> (1425)..(1425)

<223> A to G (exon 8)

<220>

<221> variation

<222> (1440)..(1440)

<223> C to T (exon 8)

<220>

<221> variation

<222> (1497)..(1497)

<223> C to T (exon 9)

<220>

<221> variation

<222> (1551)..(1551)

<223> G to A (exon 9)

<220>

<221> variation

<222> (1644)..(1644)

<223> 1381ins(C) (exon 9)

<400> 1

gagctcggcg cacctgggct gggcaggtaa gggctggtgc gggacgggga gaggaacctg	60
cagtcacctac ttgggtagag ccaggcgccc cttggctaag acgtcgagga gcgtggtagc	120
gacgggtgat cttcgctgcg gacttggttc ggagggacgt ccgcttctgg tggacagatt	180
gagcaaagaa tctttgagcg gtcaagggaa agacaagccg actcttcaga tccctgtgga	240
cacactgcct gctcttccat atc atg gcc ctc cac ccc cgc aga gtc cgg cta	293
Met Ala Leu His Pro Arg Arg Val Arg Leu	
1 5 10	
aag ccc tgg ctg gtg gcc cag gtg gat agt ggc ctc tac cct ggg ctc	341
Lys Pro Trp Leu Val Ala Gln Val Asp Ser Gly Leu Tyr Pro Gly Leu	
15 20 25	
atc tgg cta cac agg gac tct aaa cgc ttc cag att ccc tgg aaa cat	389
Ile Trp Leu His Arg Asp Ser Lys Arg Phe Gln Ile Pro Trp Lys His	
30 35 40	
gcc acc cgg cat agc cct caa caa gaa gag gaa aat acc att ttt aag	437
Ala Thr Arg His Ser Pro Gln Gln Glu Glu Glu Asn Thr Ile Phe Lys	
45 50 55	
gcc tgg gct gta gag aca ggg aag tac cag gaa ggg gtg gat gac cct	485
Ala Trp Ala Val Glu Thr Gly Lys Tyr Gln Glu Gly Val Asp Asp Pro	
60 65 70	
gac cca gct aaa tgg aag gcc cag ctg cgc tgt gct ctc aat aag agc	533
Asp Pro Ala Lys Trp Lys Ala Gln Leu Arg Cys Ala Leu Asn Lys Ser	
75 80 85 90	
aga gaa ttc aac ctg atg tat gat ggc acc aag gag gtg ccc atg aac	581
Arg Glu Phe Asn Leu Met Tyr Asp Gly Thr Lys Glu Val Pro Met Asn	
95 100 105	
cca gtg aag ata tat caa gtg tgt gac atc cct cag ccc cag ggc tcg	629
Pro Val Lys Ile Tyr Gln Val Cys Asp Ile Pro Gln Pro Gln Gly Ser	
110 115 120	
atc att aac cca gga tcc aca ggg tct gct ccc tgg gat gag aag gat	677
Ile Ile Asn Pro Gly Ser Thr Gly Ser Ala Pro Trp Asp Glu Lys Asp	
125 130 135	
aat gat gtg gat gaa gaa gat gag gaa gat gag ctg gat cag tcg cag	725
Asn Asp Val Asp Glu Glu Asp Glu Glu Asp Glu Leu Asp Gln Ser Gln	
140 145 150	
cac cat gtt ccc atc cag gac acc ttc ccc ttc ctg aac atc aat ggt	773
His His Val Pro Ile Gln Asp Thr Phe Pro Phe Leu Asn Ile Asn Gly	
155 160 165 170	
tct ccc atg gcg cca gcc agt gtg ggc aat tgc agt gtg ggc aac tgc	821
Ser Pro Met Ala Pro Ala Ser Val Gly Asn Cys Ser Val Gly Asn Cys	
175 180 185	

agc ccg gag gca gtg tgg ccc aaa act gaa ccc ctg gag atg gaa gta Ser Pro Glu Ala Val Trp Pro Lys Thr Glu Pro Leu Glu Met Glu Val 190 195 200	869
ccc cag gca cct ata cag ccc ttc tat agc tct cca gaa ctg tgg atc Pro Gln Ala Pro Ile Gln Pro Phe Tyr Ser Ser Pro Glu Leu Trp Ile 205 210 215	917
agc tct ctc cca atg act gac ctg gac atc aag ttt cag tac cgt ggg Ser Ser Leu Pro Met Thr Asp Leu Asp Ile Lys Phe Gln Tyr Arg Gly 220 225 230	965
aag gag tac ggg cag acc atg acc gtg agc aac cct cag ggc tgc cga Lys Glu Tyr Gly Gln Thr Met Thr Val Ser Asn Pro Gln Gly Cys Arg 235 240 245 250	1013
ctc ttc tat ggg gac ctg ggt ccc atg cct gac cag gag gag ctc ttt Leu Phe Tyr Gly Asp Leu Gly Pro Met Pro Asp Gln Glu Glu Leu Phe 255 260 265	1061
ggt ccc gtc agc ctg gag cag gtc aaa ttc cca ggt cct gag cat att Gly Pro Val Ser Leu Glu Gln Val Lys Phe Pro Gly Pro Glu His Ile 270 275 280	1109
acc aat gag aag cag aag ctg ttc act agc aag ctg ctg gac gtc atg Thr Asn Glu Lys Gln Lys Leu Phe Thr Ser Lys Leu Leu Asp Val Met 285 290 295	1157
gac aga gga ctg atc ctg gag gtc agc ggt cat gcc att tat gcc atc Asp Arg Gly Leu Ile Leu Glu Val Ser Gly His Ala Ile Tyr Ala Ile 300 305 310	1205
agg ctg tgc cag tgc aag gtg tac tgg tct ggg cca tgt gcc cca tca Arg Leu Cys Gln Cys Lys Val Tyr Trp Ser Gly Pro Cys Ala Pro Ser 315 320 325 330	1253
ctt gtt gct ccc aac ctg att gag aga caa aag aag gtc aag cta ttt Leu Val Ala Pro Asn Leu Ile Glu Arg Gln Lys Lys Val Lys Leu Phe 335 340 345	1301
tgt ctg gaa aca ttc ctt agc gat ctc att gcc cac cag aaa gga cag Cys Leu Glu Thr Phe Leu Ser Asp Leu Ile Ala His Gln Lys Gly Gln 350 355 360	1349
ata gag aag cag cca ccg ttt gag atc tac tta tgc ttt ggg gaa gaa Ile Glu Lys Gln Pro Pro Phe Glu Ile Tyr Leu Cys Phe Gly Glu Glu 365 370 375	1397
tgg cca gat ggg aaa cca ttg gaa agg aaa ctc atc ttg gtt cag gtc Trp Pro Asp Gly Lys Pro Leu Glu Arg Lys Leu Ile Leu Val Gln Val 380 385 390	1445
att cca gta gtg gct cgg atg atc tac gag atg ttt tct ggt gat ttc Ile Pro Val Val Ala Arg Met Ile Tyr Glu Met Phe Ser Gly Asp Phe 395 400 405 410	1493
aca cga tcc ttt gat agt ggc agt gtc cgc ctg cag atc tca acc cca	1541

Thr Arg Ser Phe Asp Ser Gly Ser Val Arg Leu Gln Ile Ser Thr Pro  
 415 420 425  
 gac atc aag gat aac atc gtt gct cag ctg aag cag ctg tac cgc atc 1589  
 Asp Ile Lys Asp Asn Ile Val Ala Gln Leu Lys Gln Leu Tyr Arg Ile  
 430 435 440  
 ctt caa acc cag gag agc tgg cag ccc atg cag ccc acc ccc agc atg 1637  
 Leu Gln Thr Gln Glu Ser Trp Gln Pro Met Gln Pro Thr Pro Ser Met  
 445 450 455  
 caa ctg ccc cct gcc ctg cct ccc cag taa ttgtgaatgc catcttcttc 1687  
 Gln Leu Pro Pro Ala Leu Pro Pro Gln  
 460 465  
 cttctctttt ttataatatt gtacatatgg atttttttat tgttttagatt taaccagctt 1747  
 ttaaatctct cttttctcta acagtgttag aagtttgtga ttctccaaat atgcctagat 1807  
 ttaaagctga ttttaatttat ggaaaaatca cccttcagac tttgcttttc tttttcaaat 1867  
 ctctaattgg tagtatgata tagcatagta gaaggagatt tggcctggga gtttggacac 1927  
 caaagttcta gctgcagctt tgcttccaat gtgacctga acaagtcctt taacctctgg 1987  
 gcttcagatt tattgcttat aaagtgaaga gattggagta gtgcctgaaa ttgcatccag 2047  
 ctttagaacg gactcaatga ctttcttcta cttgtacaag gctaaactgc ctggaacaga 2107  
 atccttctgc attgttcttg taccacattt ttcttgggtt ttgttaaagt ttctcaagc 2167  
 acta 2171

<210> 2  
 <211> 467  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Ala Leu His Pro Arg Arg Val Arg Leu Lys Pro Trp Leu Val Ala  
 1 5 10 15

Gln Val Asp Ser Gly Leu Tyr Pro Gly Leu Ile Trp Leu His Arg Asp  
 20 25 30

Ser Lys Arg Phe Gln Ile Pro Trp Lys His Ala Thr Arg His Ser Pro  
 35 40 45

Gln Gln Glu Glu Glu Asn Thr Ile Phe Lys Ala Trp Ala Val Glu Thr  
 50 55 60



Gly Lys Tyr Gln Glu Gly Val Asp Asp Pro Asp Pro Ala Lys Trp Lys  
 65 70 75 80

Ala Gln Leu Arg Cys Ala Leu Asn Lys Ser Arg Glu Phe Asn Leu Met  
 85 90 95

Tyr Asp Gly Thr Lys Glu Val Pro Met Asn Pro Val Lys Ile Tyr Gln  
 100 105 110

Val Cys Asp Ile Pro Gln Pro Gln Gly Ser Ile Ile Asn Pro Gly Ser  
 115 120 125

Thr Gly Ser Ala Pro Trp Asp Glu Lys Asp Asn Asp Val Asp Glu Glu  
 130 135 140

Asp Glu Glu Asp Glu Leu Asp Gln Ser Gln His His Val Pro Ile Gln  
 145 150 155 160

Asp Thr Phe Pro Phe Leu Asn Ile Asn Gly Ser Pro Met Ala Pro Ala  
 165 170 175

Ser Val Gly Asn Cys Ser Val Gly Asn Cys Ser Pro Glu Ala Val Trp  
 180 185 190

Pro Lys Thr Glu Pro Leu Glu Met Glu Val Pro Gln Ala Pro Ile Gln  
 195 200 205

Pro Phe Tyr Ser Ser Pro Glu Leu Trp Ile Ser Ser Leu Pro Met Thr  
 210 215 220

Asp Leu Asp Ile Lys Phe Gln Tyr Arg Gly Lys Glu Tyr Gly Gln Thr  
 225 230 235 240

Met Thr Val Ser Asn Pro Gln Gly Cys Arg Leu Phe Tyr Gly Asp Leu  
 245 250 255

Gly Pro Met Pro Asp Gln Glu Glu Leu Phe Gly Pro Val Ser Leu Glu  
 260 265 270

Gln Val Lys Phe Pro Gly Pro Glu His Ile Thr Asn Glu Lys Gln Lys  
 275 280 285

Leu Phe Thr Ser Lys Leu Leu Asp Val Met Asp Arg Gly Leu Ile Leu

290		295		300
Glu Val Ser Gly His Ala Ile Tyr Ala Ile Arg Leu Cys Gln Cys Lys				
305		310		315 320
Val Tyr Trp Ser Gly Pro Cys Ala Pro Ser Leu Val Ala Pro Asn Leu				
	325		330	335
Ile Glu Arg Gln Lys Lys Val Lys Leu Phe Cys Leu Glu Thr Phe Leu				
	340		345	350
Ser Asp Leu Ile Ala His Gln Lys Gly Gln Ile Glu Lys Gln Pro Pro				
	355		360	365
Phe Glu Ile Tyr Leu Cys Phe Gly Glu Glu Trp Pro Asp Gly Lys Pro				
	370		375	380
Leu Glu Arg Lys Leu Ile Leu Val Gln Val Ile Pro Val Val Ala Arg				
385		390		395 400
Met Ile Tyr Glu Met Phe Ser Gly Asp Phe Thr Arg Ser Phe Asp Ser				
	405		410	415
Gly Ser Val Arg Leu Gln Ile Ser Thr Pro Asp Ile Lys Asp Asn Ile				
	420		425	430
Val Ala Gln Leu Lys Gln Leu Tyr Arg Ile Leu Gln Thr Gln Glu Ser				
	435		440	445
Trp Gln Pro Met Gln Pro Thr Pro Ser Met Gln Leu Pro Pro Ala Leu				
	450		455	460
Pro Pro Gln				
465				
<210> 3				
<211> 467				
<212> PRT				
<213> Homo sapiens				
<220>				
<221> MISC_FEATURE				
<223> 5' UTR to Met				

<220>  
 <221> VARIANT  
 <222> (1)..(1)  
 <223> Met11Ile  
  
 <220>  
 <221> VARIANT  
 <222> (2)..(2)  
 <223> Ala2Val  
  
 <220>  
 <221> VARIANT  
 <222> (6)..(6)  
 <223> Arg6fs  
  
 <220>  
 <221> VARIANT  
 <222> (17)..(17)  
 <223> Gln17fs  
  
 <220>  
 <221> VARIANT  
 <222> (18)..(18)  
 <223> Val18Met  
  
 <220>  
 <221> VARIANT  
 <222> (18)..(18)  
 <223> Val18Ala  
  
 <220>  
 <221> VARIANT  
 <222> (39)..(39)  
 <223> Pro39Ala  
  
 <220>  
 <221> VARIANT  
 <222> (60)..(60)  
 <223> Trp60Gly  
  
 <220>  
 <221> VARIANT  
 <222> (61)..(61)  
 <223> Ala61Gly  
  
 <220>  
 <221> VARIANT  
 <222> (66)..(66)  
 <223> Lys66Thr  
  
 <220>  
 <221> VARIANT  
 <222> (68)..(68)  
 <223> Gln68X  
  
 <220>  
 <221> VARIANT

<222> (70)..(70)  
 <223> Gly70Arg  
  
 <220>  
 <221> VARIANT  
 <222> (76)..(76)  
 <223> Pro76Ser  
  
 <220>  
 <221> VARIANT  
 <222> (82)..(82)  
 <223> Gln82Lys  
  
 <220>  
 <221> VARIANT  
 <222> (84)..(84)  
 <223> Arg84Cys  
  
 <220>  
 <221> VARIANT  
 <222> (84)..(84)  
 <223> Arg84His  
  
 <220>  
 <221> VARIANT  
 <222> (89)..(89)  
 <223> Lys89Glu  
  
 <220>  
 <221> VARIANT  
 <222> (90)..(90)  
 <223> Ser90Gly  
  
 <220>  
 <221> VARIANT  
 <222> (92)..(92)  
 <223> Glu92X  
  
 <220>  
 <221> VARIANT  
 <222> (98)..(98)  
 <223> Asp98His  
  
 <220>  
 <221> VARIANT  
 <222> (118)..(118)  
 <223> Gln118X  
  
 <220>  
 <221> VARIANT  
 <222> (156)..(156)  
 <223> His156fs  
  
 <220>  
 <221> VARIANT  
 <222> (186)..(186)  
 <223> Cys186X

<220>  
<221> VARIANT  
<222> (192)..(192)  
<223> Trp192X

<220>  
<221> VARIANT  
<222> (212)..(212)  
<223> Ser212fs

<220>  
<221> VARIANT  
<222> (219)..(219)  
<223> Ser219fs

<220>  
<221> VARIANT  
<222> (248)..(248)  
<223> Gly248fs

<220>  
<221> VARIANT  
<222> (250)..(250)  
<223> Arg250Gln

<220>  
<221> VARIANT  
<222> (253)..(253)  
<223> Tyr253X

<220>  
<221> VARIANT  
<222> (265)..(265)  
<223> Leu265fs

<220>  
<221> VARIANT  
<222> (273)..(273)  
<223> Gln273Arg

<220>  
<221> VARIANT  
<222> (274)..(274)  
<223> Val274Ile

<220>  
<221> VARIANT  
<222> (294)..(294)  
<223> Leu294Pro

<220>  
<221> VARIANT  
<222> (297)..(297)  
<223> Val297Ile

<220>

<221> VARIANT  
<222> (320)..(320)  
<223> Lys320Glu

<220>  
<221> VARIANT  
<222> (321)..(321)  
<223> Val321Met

<220>  
<221> VARIANT  
<222> (325)..(325)  
<223> Gly325Glu

<220>  
<221> VARIANT  
<222> (345)..(345)  
<223> Leu345Pro

<220>  
<221> VARIANT  
<222> (347)..(347)  
<223> Cys347Phe

<220>  
<221> VARIANT  
<222> (369)..(369)  
<223> Phe369Ser

<220>  
<221> VARIANT  
<222> (374)..(374)  
<223> Cys374Trp

<220>  
<221> VARIANT  
<222> (388)..(388)  
<223> Lys388Glu

<220>  
<221> VARIANT  
<222> (393)..(393)  
<223> Gln393X

<220>  
<221> VARIANT  
<222> (412)..(412)  
<223> Arg412X

<220>  
<221> VARIANT  
<222> (430)..(430)  
<223> Asp430Asn

<220>  
<221> VARIANT  
<222> (461)..(461)

<223> Pro461fs

<400> 3

Met Ala Leu His Pro Arg Arg Val Arg Leu Lys Pro Trp Leu Val Ala  
1 5 10 15

Gln Val Asp Ser Gly Leu Tyr Pro Gly Leu Ile Trp Leu His Arg Asp  
20 25 30

Ser Lys Arg Phe Gln Ile Pro Trp Lys His Ala Thr Arg His Ser Pro  
35 40 45

Gln Gln Glu Glu Glu Asn Thr Ile Phe Lys Ala Trp Ala Val Glu Thr  
50 55 60

Gly Lys Tyr Gln Glu Gly Val Asp Asp Pro Asp Pro Ala Lys Trp Lys  
65 70 75 80

Ala Gln Leu Arg Cys Ala Leu Asn Lys Ser Arg Glu Phe Asn Leu Met  
85 90 95

Tyr Asp Gly Thr Lys Glu Val Pro Met Asn Pro Val Lys Ile Tyr Gln  
100 105 110

Val Cys Asp Ile Pro Gln Pro Gln Gly Ser Ile Ile Asn Pro Gly Ser  
115 120 125

Thr Gly Ser Ala Pro Trp Asp Glu Lys Asp Asn Asp Val Asp Glu Glu  
130 135 140

Asp Glu Glu Asp Glu Leu Asp Gln Ser Gln His His Val Pro Ile Gln  
145 150 155 160

Asp Thr Phe Pro Phe Leu Asn Ile Asn Gly Ser Pro Met Ala Pro Ala  
165 170 175

Ser Val Gly Asn Cys Ser Val Gly Asn Cys Ser Pro Glu Ala Val Trp  
180 185 190

Pro Lys Thr Glu Pro Leu Glu Met Glu Val Pro Gln Ala Pro Ile Gln  
195 200 205

Pro Phe Tyr Ser Ser Pro Glu Leu Trp Ile Ser Ser Leu Pro Met Thr

210		215		220
Asp Leu Asp Ile Lys Phe Gln Tyr Arg Gly Lys Glu Tyr Gly Gln Thr				
225		230		235
Met Thr Val Ser Asn Pro Gln Gly Cys Arg Leu Phe Tyr Gly Asp Leu				
	245		250	255
Gly Pro Met Pro Asp Gln Glu Glu Leu Phe Gly Pro Val Ser Leu Glu				
	260		265	270
Gln Val Lys Phe Pro Gly Pro Glu His Ile Thr Asn Glu Lys Gln Lys				
	275		280	285
Leu Phe Thr Ser Lys Leu Leu Asp Val Met Asp Arg Gly Leu Ile Leu				
	290		295	300
Glu Val Ser Gly His Ala Ile Tyr Ala Ile Arg Leu Cys Gln Cys Lys				
305		310		315
Val Tyr Trp Ser Gly Pro Cys Ala Pro Ser Leu Val Ala Pro Asn Leu				
	325		330	335
Ile Glu Arg Gln Lys Lys Val Lys Leu Phe Cys Leu Glu Thr Phe Leu				
	340		345	350
Ser Asp Leu Ile Ala His Gln Lys Gly Gln Ile Glu Lys Gln Pro Pro				
	355		360	365
Phe Glu Ile Tyr Leu Cys Phe Gly Glu Glu Trp Pro Asp Gly Lys Pro				
370		375		380
Leu Glu Arg Lys Leu Ile Leu Val Gln Val Ile Pro Val Val Ala Arg				
385		390		395
Met Ile Tyr Glu Met Phe Ser Gly Asp Phe Thr Arg Ser Phe Asp Ser				
	405		410	415
Gly Ser Val Arg Leu Gln Ile Ser Thr Pro Asp Ile Lys Asp Asn Ile				
	420		425	430
Val Ala Gln Leu Lys Gln Leu Tyr Arg Ile Leu Gln Thr Gln Glu Ser				
	435		440	445



Trp Gln Pro Met Gln Pro Thr Pro Ser Met Gln Leu Pro Pro Ala Leu  
450 455 460

Pro Pro Gln  
465

<210> 4  
<211> 19  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> 870del(CACTAGCAAGCTGCTGGAC)lns  
(A)

<400> 4  
cactagcaag ctgctggac

19